

SEARCH REQUEST FORM

Scientific and Technical Information Center

Access DB# 106320

Requester's Full Name: Devi Examiner #: 24493 Date: 10/29/03
 An Unit: 1645 Phone Number 308-9347 Serial Number: 0915905991
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Search seq 6 against aaw61246

with alternate scoring tables

Find AAW61246 in

PCT/US97/19422

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Type of Search		Vendors and cost where applicable
Searcher: <u>D. Schreiber</u>	NA Sequence (#) _____	STN: _____
Searcher Phone #: <u>308-4292</u>	AA Sequence (#) <u>4</u>	Dialog: _____
Searcher Location: <u>CMC CAO3</u>	Structure (#) _____	Questel Orbit: _____
Date Searcher Proposed: _____	Bibliographic: _____	On Line: _____
Date Completed: <u>10/21</u>	Litigation: _____	Lexis Nexis: _____
Searcher Prep & Review Time: <u>21</u>	Fulltext: _____	Sequence Systems: <u>Comp 4903</u>
Client Prep Time: _____	Patent Family: _____	MANA Internet: _____
Indexing Time: <u>27</u>	Other: _____	Other: _____

See ID NO. 6

ESULF 3
AM61246
D AM61246 standard; Protein: 1007 AA.
X
C AM61246;
X
T 02-OCT-1998 (first entry)
X
E Streptococcus pneumoniae SPI22 protein.
X
M Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;
X detection; pneumonia; otitis media; meningitis.
X
S Streptococcus pneumoniae.
X
N WO9818930-A2.
X
D 07-MAY-1998.
X
F 30-OCT-1997; 97WO-US19422.
X
R 31-OCT-1996; 96US-0029960.
X
A (HUMA-) HUMAN GENOME SCI INC.
X
I Chol GH, Hromocky J A, Johnson LS, Kunsch CA;
X
R MPI: 1998-272224/24.
X
R N-PSDB: AAV27431.
X
T Nucleic acid encoding antigenic peptide(s) from Streptococcus
T pneumoniae - or their epitope-containing fragments, useful in
T protective or therapeutic vaccines, and for diagnosis
X
S Claim 11, Page 92-93; 118pp; English.

CC The present sequence represents a protein from Streptococcus pneumoniae.
CC The nucleic acid sequence encoding the Streptococcus pneumoniae protein
CC can be useful in vaccines for inducing protective antibodies against
CC Streptococcus pneumoniae, for treatment or prevention of infection e.g.
CC pneumonia, otitis media or meningitis. Probes based on the nucleic acid
CC are used to detect Streptococcus infection (by usual hybridisation or
CC amplification methods), also for isolating Streptococcus genes or their
CC allelic variants. The protein can be used similarly to detect specific
CC antibodies in standard immunoassays, especially for diagnosing or
CC monitoring infections. Antibodies which bind the protein and for passive
CC detect corresponding antigens, to purify the protein and for passive
CC immunisation (optionally coupled to a toxin). Vaccines are administered,
CC e.g. by injection, orally or through the skin, typically at 0.01-1000
CC (especially 10-300) mu g/ml per dose.
XX
XX Sequence 1007 AA:

Query Match 94.6%; Score 3269; DB 19; Length 1007;
Best Local Similarity 100.0%; Pred. No. 8.2e-184;
Matches 627; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 ETSODFREKKTAVIKKEKYVSKNPVIDNNTSNEAKIKENSKSGDYTDSPVKNTEEN 97
DB 1 etsqdlfekkktavikekevsknpvidnntseakikeensnsgdytdspvknnten 60
QY 98 PKKEDKVVYIAEFKDESGEKAIKELSLKNTKVLTYDRIFGNSAIEETPPNLDKIKOI 157
DB 61 pkkedkvvyiaefkdesgekalkelslknktvlytdrlfngsaletppnldkikoi 120
QY 158 EGISVERAOKVOPMNHAKKEIGVEAIDYLSKSNAPGKNFDGNGMYISNIDTDTDR 217
DB 121 egisveraokvopmnhakkeigveaidylsksnapgnfdgngmyisnidtdtgyr 180
QY 218 HKAMRIDDOAKASMRKEDLKTGDKRWYLSDKIRHAFNYYNGSKITVEYDGRDYPDP 277
DB 181 hkamriddoakasmrkedlktgdkrwylsdkirhafnynyngskitveydgrdydp 240
QY 278 HGMHIGILAGNPEDIDKFNFGIDGIAFNAQIFSYKMYSDAGSGFAGDETFMAIEDSI 337
DB 241 hgmlhigilagnpedidkfnfgidgialfnaqifsykmysdagsgfagdetfmhaiedsi 300
QY 338 KHNVDVSVSGFTGTGLVGEKYQWAIKALRKAGIPMVAATGNYATSASSSSNDLVANNH 397
DB 301 khndvsvsgftgtglvgekyqwaikalkrkgipmvatgnyatsassssndlvannh 360
QY 398 LKMTDTGNVTRTAHEDALIVASAKNOTVEBDKYNIGSGSFRTNIGAFPDASKITTNED 457
DB 361 lkmtdtgnvtrtahedalivasaknotvebdkynigsgsftrnigafpdaskittned 420
QY 458 GTRAPSKLAFYIIGKGDODLIGDLRGKTAVMDRITKDLKNAFKKAMKGARAIMVYN 517
DB 421 gtrapsklafyigkgdodligrkgtavmdritkdlknafkamkgaraimvyn 480
QY 518 TVNYNDRDNTLPAWGYEADDEGTSQVFSISGDGKVLNMMINPDKTEVKRNKEDFK 577
DB 481 tvnyndrdntlpaawyeaddegtsqvfissgdgkvlmmiinpdktevkrnkedfk 540
QY 578 DKLEOYYPIDMESFNSNKNPNVDEKEIDFKFAPDTDELYKEDIIVAGSTSWGPRIIDL 637
DB 541 dkleyypidmesfnsnknpnvdekeidfkfapdtdekykediivagstswgpridil 600
QY 638 LKPYVASGKNKIKSTLVNINCKSTYCY 664
DB 601 lkpyvasgknkikstlvninckstycy 627

SEE D NO: 6

RESULT 2

0984M8 ID 0984M8 PRELIMINARY; PRT: 2144 AA.

AC 0984M8; 01-MAY-2000 (TEMBLrel. 13, Created)

DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)

DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)

DE CELL WALL-ASSOCIATED SERINE PROTEINASE PRECURSOR PRTA.

GN PRTA.

OS Streptococcus pneumoniae.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;

OC Streptococcus.

OX NCBI_TaxId=1313;

RN (1)

RP SEQUENCE FROM N.A.

RA STRAIN-3.B;

RC Betha G., ten Thoren E., Bongaerts R.J.M., Heinz H.-P., Zysk G.;

RT *Cloning and sequencing of a novel surface protease of Streptococcus

RT pneumoniae.*;

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF127143; AAD48399.1; -

DR HSP: P07518; IME.

DR InterPro: IPR001899; Gram_pos_anchor.

DR InterPro: IPR001337; PA.

DR InterPro: IPR00209; Peptidase_S8.

DR Pfam: PF00746; Gram_pos_anchor; 1.

DR Pfam: PF02225; PA; 1.

DR PRINTS: PR00723; SUBTILISIN.

DR PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.

DR PROSITE: PS00137; SUBTILASE_HIS; UNKNOWN_1.

DR PROSITE: PS00138; SUBTILASE_SER; UNKNOWN_1.

DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_1.

KM SIGNAL.

FT SIGNAL. 1 19 POTENTIAL.

FT CHAIN 20 2144 CELL WALL-ASSOCIATED SERINE PROTEINASE

FT CHAIN PRTA

SEQUENCE 2144 AA: 240725 MW: 2052511470741331 CRC64;

Query Match 96.8%; Score 3142.5; DB 2; Length 2144;

Best Local Similarity 96.3%; Pred. No. 4.1e-168;

Matches 642; Conservative 14; Mismatches 6; Indels 5; Gaps 1;

0y 3 VVLADTSSSEDLNLSDEKV-----AEKKEHENHSHAMETSDOFKKEKTAVKEKEV 57

Db 24 VVLADTSSSEDLNLSDEKVYVDKETEKKKHNDIHAITSKDEKKTITIEKEV 83

0y 58 SKNPVIDNNTSNEEKIKEENSNSQGDYDTSFVNKNTENPKKEDKVYVIAEFKKESE 117

Db 84 SKNPVIDTKTSNEEKIKEENSNSQGDHDSFVNKNTENPKKEDKVYVIAEFKKESE 143

0y 118 KAIKELSLKNTKVLTYDRIFGNSAIEETPDNDIKIKOIGISSVERAOKVPMNHAR 177

Db 144 KAIKGLSLKNTKVLTYDRIFGNSAIEETPDNDIKIKOIGISSIERAOKVPMNHAR 203

0y 178 KEIGVEEALDYKLSINAPFGKNGFDGRGVISNIDGTDRHKAARRIDDAKASMRKED 237

Db 204 KEIGVEEALDYKLSINAPFGKNGFDGRGVISNIDGTDRHKAARRIDDAKASMRKED 263

0y 238 LKGTDKNWLSDKIPHAFNYNGKTIKVEKYDDGRDYFDPHGHAGIAGNDTEODIRN 297

Db 264 LKGTDKNWLSDKIPHAFNYNGKTIKVEKYDDGRDYFDPHGHAGIAGNDTEODIRN 323

0y 298 FNGIDGIAPNAQIFSKMYSDAGSGFAGDETHAIEDSKHNVDSVSSGFTGLVG 357

Db 324 FNGIDGIAPNAQIFSKMYSDAGSGFAGDETHAIEDSKHNVDSVSSGFTGLVG 383

0y 358 EKYWOAIRALKRAGIPMVATGNYATSASSSHDLVANNHLKMTDGNTRTAHEDAIA 417

Db 384 EKYWOAIRALKRAGIPMVATGNYATSASSSHDLVANNHLKMTDGNTRTAHEDAIA 443

0y 418 VASAKNOTVEFDKVNIGSGSFKRNIGAEFDKSKITTNEGTAKAPSKLFEVYIGGODD 477

Db 444 VASAKNOTVEFDKVNIGSGSFKRNIGAEFDKSKITTNEGTAKAPSKLFEVYIGGODD 503

0y 478 LIGLDLRGKIAVDRITYTDLKNAPKAMDKARALMVNTVNYNRDMTELPMAGYEA 537

Db 504 LIGLDLRGKIAVDRITYTDLKNAPKAMDKARALMVNTVNYNRDMTELPMAGYEA 563

0y 538 DEGTSSOVFSISGDDGVKLMMNINPDKTEVRNNKEDKDLQYIYIDESHFNKPN 597

Db 564 DEGTSSOVFSISGDDGVKLMMNINPDKTEVRNNKEDKDLQYIYIDESHFNKPN 623

0y 598 VGDEKEIDFKFAPDPTDKELYEDIIIVPAGSTSWGPRIDLKPDVSAGKNIKSTLVIN 657

Db 624 VGDEKEIDFKFAPDPTDKELYEDIIIVPAGSTSWGPRIDLKPDVSAGKNIKSTLVIN 683

0y 658 GKSTGY 664

Db 684 GKSTGY 690